AAGCTCAGAT CTACCTGCCT GAGGGCGTCC GGTTCCAGCT GGCCCTTCCC GAGGGGGAGA	60
GGGAGGCGTT TCTAAAAGCC CTTCAGGACG CTACCCGGGG GCGGGTGGTG GAAGGGTAAC	120
ATG AGG GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu 1 15	168
GTG GAC GGC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly 20 25 30	216
CTC ACC ACC AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala 35 40 45	264
AAG AGC CTC CTC AAG GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val 50 60	312
GTC TTT GAC GCC AAG GCC CCC TCC TTC CGC CAC GAG GCC TAC GGG GGG Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly 65 70 75 80	360
TAC AAG GCG GGC CGG GCC CCC ACG CCG GAG GA	408
GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG CTG GCG CGC CTC GAG Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu 100 105	456
GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG GCC AAG AAG Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys 115	504
GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA GAC Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp 130 135	552
CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly 145 150 160	600
TAC CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro 165 170 175	648
GAC CAG TGG GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn 180 185	696
CTT CCC GGG GTC AAG GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu 195 200 205	744

FIG. 1A

GAG Glu	GAG GLu 210	TGG Trp	GGG Gly	6 A(	GC ( er l	LCu	GAA Glu 215	GCC Ala	CTC Leu	CTC Leu	A L	AG ys	AAC Asn 220	CTG Leu	G.	AC SD	CGG Arg	CTG Leu	792
AAG Lys		GCC Ala	ATO	C C	GG (	GAG Glu 230	AAG Lys	ATC Ile	CTG Leu	GCC Ala	C H 2	AC is 35	ATG Met	GAC Asp	G	AT SD	CTG Leu	AAG Lys 240	840
				C C		000		CTC	CGC Arg	<b>VCC</b>	G	ΔC	CTG	$\mathbb{CCC}$	C	TG	GAG	616	888
GAC Asp	TTC Phe	GCC Ala	AA Ly 26	A A s A		CGG Arg	GAG Glu	CCC Pro	GAC Asp 265	CGG	; G	AG lu	AGG Arg	CT1 Let	- A	GG Arg 270	GCC Ala	TTT Phe	936
CTG Leu	GAG Glu	AGG Arg 275	CT Le		SAG Slu	TTT Phe	GGC Gly	AGC Ser 280	CTC Leu	CT( Let	) ( ) H	CAC	GAG Glu	TT( Phe 28!		GGC Glu	CTT Leu	CTG Leu	984
GAA Glu	Ser	CCC		G G	GCC Ala	CTG Leu	GAG Glu 295	Ulu	GCC Ala	CC( Pro		TGG Trp	CCC Pro 300	CC( Pr	G (	CCG Pro	GAA Glu	GGG Gly	1032
Ala	Phe	GT(	G G G	GC T	TTT Phe	GTG Val 310	CTT	TCC	CGC Arg	AA Ly	G (	GAG Glu 315	CCC Pro	AT Me	G :	TGG Trp	GCC Ala	GAT Asp 320	1080
305 CTT Let		GC(	C CT a Le	rg (	GCC Ala	ccc	GCC Ala	AGG Arg	G GGG G G I y	GG G1 33	۲.	CGG	GTO	: CA	С	CGG	GCC	CCC	
									· CT(	٠ ۸ ۸	c	GAG	GCG	: re	G	GGG	CTT	CTC Leu	1176
			C C				·		CTO a Lei	. AG		CAA	GGG	רח ר	T	GGC	CTO	CCG	1224
CC Pr	o Gli	C GA y As		AC SD	CCC Pro	AT(	G CT t Le 37	C CT	c cc	C TA a Ty	C /r	CTC Let	CTO Leo 38	G G/ u As	AC SP	CCT	TC( Se	C AAC r Asr	1272
AC Th	37 C AC r Th		C G	AG lu	GGG Gly	GT( Va		~ ~ ~ ~	G CG g Ar	C TA	YC YC	GG( G1) 395	C GG y G1	G G	AG lu	TG(	S AC	G GA( r Gl) 400	3 1320 1
						G GC		c cT	T TC	C G/	۸С	AGO	c CT	CT	TC	GCC	C AA	C CTI n Lei 5	G 1368
TG Tr	66 66 19 G1	G A(	GG ( rg l	CTT Leu 420			G GA y Gl	iG GA u Gl	G AG U Ar 42	iG Ci ig L	TC eu	CT Le	T TG u Tr	G C	TT eu	TA Ty 43	C CG r Ar O	G GA g Gl	G 1416 u

FIG. 1B

GTG Val	GAG Glu	AGG Arg 435	CCC Pro	CTT Leu	TCC Ser	GCT Ala	GTC Val 440	CTG Leu	GCC Ala	CAC His	ATG Met	GAG Glu 445	GCC Ala	ACG Thr	GGG Gly	1464
GTG Val	CGC Arg 450	CTG Leu	GAC Asp	GTG Val	GCC Ala	TAT Tyr 455	CTC Leu	AGG Arg	GCC Ala	TTG Leu	TCC Ser 460	CTG Leu	GAG Glu	GTG Val	GCC Ala	1512
GAG Glu 465	GAG Glu	ATC Ile	GCC Ala	CGC Arg	CTC Leu 470	GAG Glu	GCC Ala	GAG Glu	GTC Val	TTC Phe 475	CGC Arg	CTG Leu	GCC Ala	GGC Gly	CAC His 480	1560
CCC Pro	TTC Phe	AAC Asn	CTC Leu	AAC Asn 485	TCC Ser	CGG Arg	GAC Asp	CAG Gln	CTG Leu 490	GAA Glu	AGG Arg	GTC Val	CTC Leu	TTT Phe 495	GAC Asp	1608
GAG Glu	CTA Leu	GGG Gly	CTT Leu 500	CCC Pro	GCC Ala	ATC Ile	GGC Gly	AAG Lys 505	ACG Thr	GAG Glu	AAG Lys	ACC Thr	GGC- Gly 510	AAG Lys	CGC Arg	1656
TCC Ser	ACC Thr	AGC Ser 515	GCC Ala	GCC Ala	GTC Val	CTG Leu	GAG Glu 520	GCC Ala	CTC Leu	CGC Arg	GAG Glu	GCC Ala 525	CAC His	CCC Pro	ATC Ile	1704
GTG Val	GAG Glu 530	AAG Lys	ATC Ile	CTG Leu	CAG Gln	TAC Tyr 535	CGG Arg	GAG Glu	CTC Leu	ACC Thr	AAG Lys 540	CTG Leu	AAG Lys	AGC Ser	ACC Thr	1752
TAC Tyr 545	ATT Ile	GAC Asp	CCC Pro	TTG Leu	CCG Pro 550	GAC Asp	CTC Leu	ATC	CAC His	CCC Pro 555	AGG Arg	ACG Thr	GGC Gly	CGC Arg	CTC Leu 560	1800
CAC His	ACC Thr	CGC Arg	TTC Phe	AAC Asn 565	CAG Gln	ACG Thr	GCC Ala	ACG Thr	GCC Ala 570	ACG Thr	GGC Gly	AGG Arg	CTA Leu	AGT Ser 575	AGC Ser	1848
TCC Ser	GAT Asp	CCC Pro	AAC Asn 580	CTC Leu	CAG Gln	AAC Asn	ATC Ile	CCC Pro 585	GTC Val	CGC Arg	ACC Thr	CCG Pro	CTT Leu 590	GGG Gly	CAG Gln	1896
AGG Arg	ATC Ile	CGC Arg 595	Arg	GCC Ala	TTC Phe	ATC Ile	GCC Ala 600	GAG Glu	GAG Glu	GGG Gly	TGG Trp	CTA Leu 605	TTG Leu	GTG Val	GCC Ala	1944
CTG Leu	GAC Asp 610	Tyr	AGC Ser	CAG Gln	ATA Ile	GAG Glu 615	CTC Leu	AGG Arg	GTG Val	CTG Leu	GCC Ala 620	CAC His	CTC Leu	TCC Ser	GGC Gly	1992
GAC Asp 625	Glu	AAC Asn	CTG Leu	ATC Ile	CGG Arg 630	Val	TTC Phe	CAG Gln	GAG Glu	GGG Gly 635	CGG Arg	GAC Asp	ATC Ile	CAC	ACG Thr 640	2040
GAG Glu	ACC Thr	GCC Ala	AGC Ser	TGG Trp 645	ATG Met	TTC Phe	GGC Gly	GTC Val	CCC Pro 650	CGG Arg	GAG Glu	GCC Ala	GTG Val	GAC Asp 655	Pro	2088

FIG. 1C

CTG Leu	ATG Met	CGC Arg	CGG Arg 660	GCG Ala	GCC Ala	AAG Lys		ATC Ile 665	AAC Asn	TTC Phe	GGG Gly	GTC Val	CTC Leu 670	TAC Tyr	GGC Gly	2136
ATG Met	TCG Ser	GCC Ala 675		CGC Arg	CTC Leu	TCC Ser	CAG Gln 680	GAG Glu	CTA Leu	GCC Ala	ATC Ile	CCT Pro 685	TAC Tyr	GAG Glu	GAG Glu	2184
Ala	CAG Gln 690	GCC Ala	Pne	116	GIU	695	ועו	1 110	0111		700					2232
GCC Ala 705	TGG Trp	116	e Glu	Ly5	710	LCu	UTU	010	0.,	715					/20	2280
GA(	G ACC u Thr	Let	ı Phe	160	AIG	AIG	AIG	, , ,	730					735		2328
GT Va	G AAG	AG( S Sei	C GT( r Va) 740	l Aly	GAG Glu	GCG Ala	GCC Ala	GAG Glu 745	CGC Arg	ATG Met	GCC Ala	TTC Phe	AAC Asr 750	: ATG Met	CCC Pro	2376
Va	1 G11	1 61 75	y in: 5	r Ala	HIO	H N N	760	1100			–	765	5		CTC Leu	2424
TT Ph	C CC ne Pri	C AG		G GAG u Glu	GAA Glu	ATO Met 775		GCC Ala	AGG Arg	ATG Met	CT( Let 780	CTT Let )	CA( JGl	G GTO n Val	CAC	2472
A 9	AC GA	G CT u Le	u va	1 Lei	790	) "1	<b>3</b> 110	, .,		79	5				G GCC I Ala 800	2520
C	GG CT rg Le	G GC	C AA la Ly	G GA S G1 80	G GT u Va 5	C AT	G GAG t Gl	G GGG U Gl	G GT y Va 81	G TA' 1 Ty 0	T CC r Pr	C CT o Le	G GC u Al	C GT a Va 81	G CCC 1 Pro 5	2568
C L	TG GA eu Gl	NG G	TG GA al Gl 82	lu va	G GG l Gl	G AT y Il	A GG e Gl	G GA y Gl 82		C TG p Tr	G CT p Le	C TC u Se	C GC r Al 83	C AA a Ly SO	G GAG s Glu	2616
Т	GATA	CCAC	С													2626

FIG. 1D

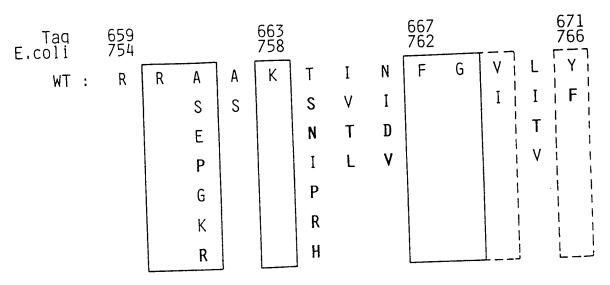


FIG. 2A

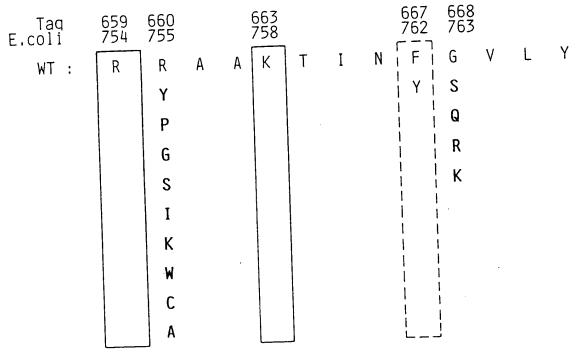


FIG. 2C

Taq E.coli	659 754				663 758				667 762			í	671 766	
Taqi Taqi Taqi Taqi Taqi Taqi Taqi Taqi	659 754 R	R	A S ERTP R S G EPP	A S SS	663 758 K	TPP SASRLS IRS K PSN S I N	I V	N D I I I I I	667 762 F	G	V I I I T	T T	671 766 Y	
308 : 308 : 44 : 54 : 110 : 219 : 250 : 30 : 156 :	Q		P T E G P	G		RP PSRS	T V T T V	Y I I	L		I	V	F         	

FIG. 2B

AACAGCTATG ACC ATG ATT ACG AAT TCA CTG GCC GTC GTT TTA CAA CGT CGT +80 +80 TITATGCTTC CGGCTCGTAT GTTGTGGGCG GATAACAATT TCACACAGGA +11 +20 S' - GCGCA ACGCAATTAA TGTGAGTTAG CTCACTCATT AGGCACCCCA GGCTTTACAC

T C A CC CCT GGC GTT ACC CAA CTT AAT CGC CTT GCA GCA CAT CCC +120

CCT TTC GCC AGC TGG CGT AAT AGC GAA GAG GCC CGC ACC GAT CG +140

FIG. 3